

# GSCF User Guide

## Introduction - GSCF

GSCF (Generic Study Capture Framework) is a web application that is designed to store the design of biological studies in a database. GSCF serves as a linking hub for other modules: it links to the data in the various assay modules.

So, before data in modules can be entered, the study design needs to be in GSCF. The following image (headers) illustrates what type of information can be stored in GSCF.

Show Study

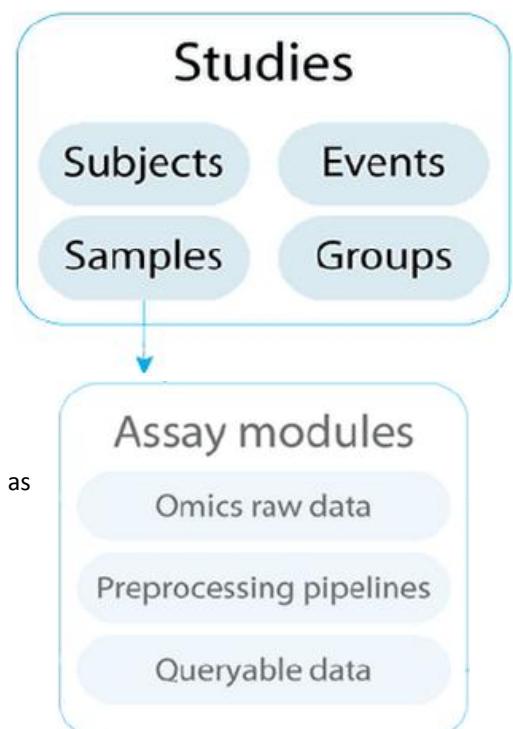
Study Information	Subjects	Events timeline	Events table	Assays	Samples	Persons	Publications
title PPS3							
description Excessive intake of dietary fat is known to be a contributing factor in the development of obesity. In this study, we determined the dose-dependent effects of dietary fat on the development of this metabolic condition with a focus on changes in gene expression in the small intestine. C57BL/6 mice were fed diets with 10, 20, 30, or 45 energy% (E%) derived from fat, as well as a control diet (n=10 mice/diet). We found a significant high weight gain in mice fed the 30 and 45% fat diet compared to mice on the control diet. These data indicate that the main shift towards an obese phenotype lies between a 20% and 30% dietary fat intake. Analysis of differentially gene expression in the small intestine showed a fat-dose dependent gradient in differentially expressed genes, with the highest numbers in mice fed the 45% fat diet. The main shift in fat-induced differential gene expression was found between the 30% and 45% fat diet. Furthermore, approximately 70% of the differentially expressed genes were regulated in a fat-dose dependent manner. Many of these genes were involved in lipid metabolism-related processes and were already differentially expressed on a 30% fat diet. Taken together, we conclude that up to 20% of dietary fat, the small intestine has an effective 'buffer capacity' for fat handling. From 30% of dietary fat, a switch towards an obese phenotype is triggered. We further speculate that especially fat-dose dependently regulated lipid metabolism-related genes are involved in development of obesity.							
code NuGO_PPS3							
startDate 2008-04-01 00:00:00.0							

## Introduction – assay modules

Users can create samples by their study design in GSCF, and indicate where the assay data is stored. In these assay modules users can easily import, for example bulks of numerical data, from Excel files. The following modules are currently available for GSCF:

- Metagenomics
- Clean transcriptomics (CTD)
- Metabolomics
- Simple Assay Module (SAM)
- Transcriptomics

For example, the Simple Assay Module (SAM) is used to store clinical data, such as Rules Based Medicine assays, but also physical measurements such as body weight of mice. The image below illustrates how GSCF and assay modules are related.



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# Tips and tricks

## General

- ✓ Use 'import study data' to import large datasets (for example: many subjects) from an excel sheet into your study (see also Chapter 1.3 Import part of study design).
- ✓ When you want to use Advanced search, and choose *sample* as the output format, note that this search can take several minutes, since the number of samples could be very high.

## Study wizard

- ✓ Use next and previous (at the bottom of the page) to navigate, or use 'quick save' at any time during the wizard, to complete it at another point in time.



A screenshot of a web-based study wizard. At the bottom, there is a navigation bar with '« prev', 'quick save' (which is circled in green), and 'next »'. Below the navigation bar, a copyright notice reads 'Copyright © 2008 - 2012 NuGO, NMC and NBIC. All rights reserved.'

- ✓ Hovering over question marks will show additional information on required fields: 
- ✓ Use the upper left icon to select all rows in a table:



A screenshot of a table with a blue header row labeled 'Name'. The first row contains the value '200'. The second row contains '201', the third '202', and the fourth '203'. The table has a vertical scrollbar on the right.

- ✓ Select multiple rows by click and dragging over multiple rows:



A screenshot of a table titled 'Human template'. The first nine rows are selected, as indicated by a red background. The columns are labeled 'Name' and 'species'. The 'Name' column contains values 1 through 9, and the 'species' column contains 'Homo sapiens' for all rows.

## 1. Getting started – simple import and wizard

Using the menu on top of the application, you can either create, view or import studies and study data.

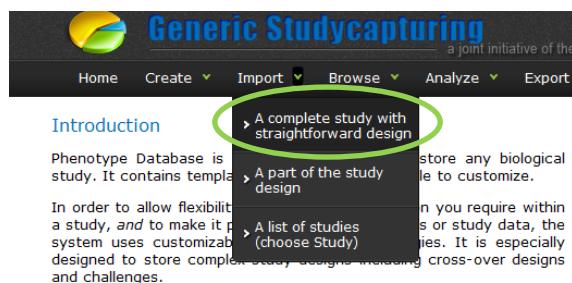
Generally, there are two ways to get your data into the database.

1. Start the study *wizard*, which will guide you step-by-step. This will allow you to describe the study design, all events and sampling events that take place, and on what time. Also into what event groups your subjects are organized. Based on subjects, event groups and events, GSCF will create samples. Samples are the links between GSCF and the assay modules, where you can store specific data (such as metabolomics or clinical chemistry values). (Go to chapter 1.1 for a more detailed description.)

*Advantage: full description of your study design, and easy to compare with other GSCF-created studies that are fully described.*

*Disadvantage: because a lot of information can be stored to describe your study, it takes some time before you can start using the modules. Especially when your study contains a lot of samples (>1000), the wizard can become a bit slow.*

2. a. If you have a sample list of all samples in your study, you can use the *short way* to get data into the system. Since samples/samplenames are the link between GSCF and the assay modules, you can simply create a study, and describe study metadata.



- b. Then use the importer (Import > A part of study design) to import your Excel sheet, and thereby import your own sample names. These names can then be used in the various assay modules, to add metabolomics data. (Go to chapter 1.3 for a more detailed description.)

*Advantage: you can quickly enter data into the module, since only minimal necessary information is imported.*

*Disadvantage: comparing two studies is more difficult if users only fill in minimal study (meta)data.*

- ➔ Use the content list on page 2, to navigate through this guide
- ➔ For any questions that could not be answered through this guide, please email [support@thehyve.nl](mailto:support@thehyve.nl)

## 1.1 Create a new study (wizard)

For creating a new study, you have to have a login. See chapter 7 ( Access control) on how to become a user. Click on Create > Create a new study using the menu on top. This will start the 6-step study wizard.

### Step 1: Start



Define basic properties of your study. Fields indicated by an arrow are required.

You can choose an appropriate template, or create a new template. This will allow you to add and modify fields.

Template	<a href="#">add / modify...</a>
Title	
Description	
Code	<a href="#">Mass-Sequencing Study</a>
Start Date	
Published Publications	<a href="#">Test study</a>
Contacts	<a href="#">human intervention</a>
	<a href="#">mice intervention study</a>
	<a href="#">add / modify...</a>
	<a href="#">No publications selected</a>
	<a href="#">Add Publication</a>
	<a href="#">No contacts selected</a>

In some browsers (Firefox 4, Safari and Chrome) fields can be enlarged by dragging the indicated (lower right) corner of the text field.

### Step 2: Subjects



Use this step to manually add a number of subjects: report the number of subjects in your study and choose the template. Then add these subjects to your study and fill out the required information in the table.

Number Of Subjects To Add	<input type="text" value="11"/>
Of Species	<input type="text" value="Homo sapiens"/>
With Template	<input type="text" value="Human"/>
	<a href="#">Add</a>

Human template

Name	Species	Individ. Id	Gender	Age (Years) (years)
1	Homo sapiens		Male	0
2	Homo sapiens		Female	0
3	Homo sapiens		Female	0
4	Homo sapiens		Male	0

If you have an excel file with subject list, a separate importer can be used. Especially, when you have detailed subject information, this importer can be used very efficiently. See Topic 3 - Import part of study design (page 10).

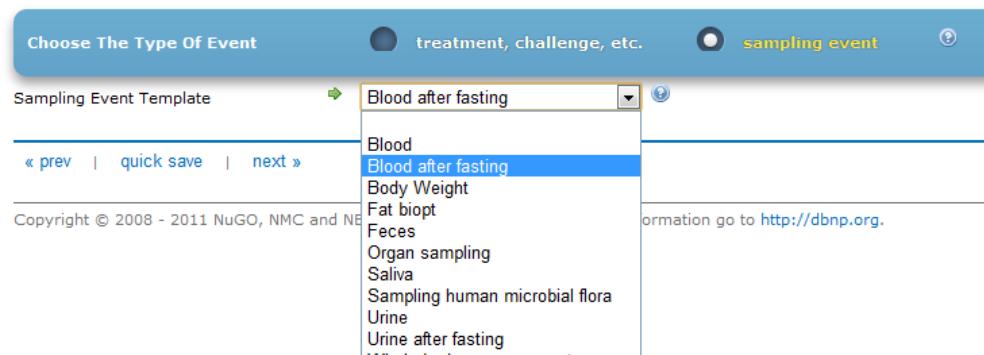
### Step 3: (Sampling) Events



Any treatment, challenge or occurrence in your study can be defined in the events step. An *event* is defined as anything that happens to subject(s) in your study that is not resulting in a sample. Whereas *sampling events* if the event results in extraction of samples, where you want to store measurements upon. First choose between treatment or sampling event:



Then choose the appropriate (sampling) event template:



After you have added an event or sampling event, it will appear in a list below, and you can modify this event if necessary. Here, you also need to create any event *groups* that occur in your study. Make sure that each event is linked to a group. Only then subjects can be added into this group (see next step).

- Important: each event should be added separately.
- Important: a combination of sampling events, subjects and groups, will automatically create samples.

	Group 1	Group 2	Start Time	Duration	Sample Template	Control
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	0s	0s	Blood	Y
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	1w	0s	Blood	Y
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	2w	0s	Blood	Y

## Subjects into event groups

Click next: this in-between-step allows you to select subjects and indicate to which event group they belong.

Subjects	Group 1	Group 2
Human		
Subject 1	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 2	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 3	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 4	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 5	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 6	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Subject 7	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Subject 8	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Subject 9	<input type="checkbox"/>	<input checked="" type="checkbox"/>

➤ Note: event groups are created in Step 3. You can fill these groups with subjects between Step 3 and 4.

## Step 4: Samples

1. Start ➤ 2. Subjects ➤ 3. Events ➤ 4. Samples ➤ 5. Assays ➤ 6. Confirmation ➤ 7. Done

This step gives a table with all the samples that were created. Note that a combination of sampling events, subjects and groups, automatically created your samples.

You can make any adjustments, or fill out empty fields when necessary.

## Step 5: Assays

1. Start ➤ 2. Subjects ➤ 3. Events ➤ 4. Samples ➤ 5. Assays ➤ 6. Confirmation ➤ 7. Done

In this step assays can be created. Depending on the assay type and module you choose, later on you can attach measurements or data files to a set of samples.

Make sure to select the template (e.g. clinical chemistry), fill in an assay name and select the module (e.g. simple assay module) you wish to use.

Template	<input type="text" value="Clinical Chemistry"/>
Name	<input type="text" value="blood_clinchem"/>
Module	<input type="text" value="simple assay module"/>
Clinical Chemistry Platform	<ul style="list-style-type: none"><li>Metagenomics</li><li>clean transcriptomics database</li><li>metabolomics</li><li><b>simple assay module</b></li></ul>

## Samples into Assays

After you click 'next', an in-between step allows you to select which assays were performed on which samples. Select multiple rows by click and dragging. Use checkboxes to indicate to what assay these samples belong.

(It is possible to attach multiple assay to one sample.)

Sample Type	Sample Name	blood_clinchem	blood_transcr
Blood	Subject1_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject10_Blood_Group2_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject11_Blood_Group2_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject2_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>
	Subject3_Blood_Group1_0sBlood	<input checked="" type="checkbox"/>	<input type="checkbox"/>

## Step 6: Confirmation



Check your data. Any corrections can be made by going back to the corresponding steps in the wizard.

## Step 7. Done

You can view or edit the newly created study, or create a new study.

## 1.2 Edit a study

To view or edit an already existing study go to Browse > My studies.



Now you see a list of studies that you have created, or studies where you have the role of reader. Click on the magnifying glass on the left to view a certain study, or click on the pencil in the middle to enter the wizard. This will allow you to edit this study.

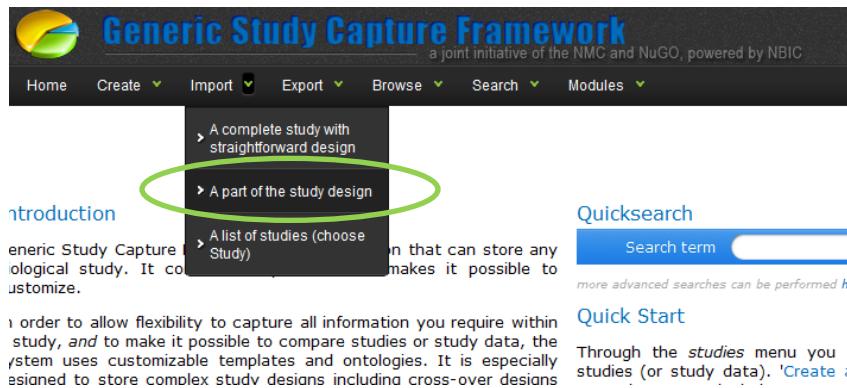
Study List									
		Code	Title	Subjects	Events	Assays			
<input type="checkbox"/>					codeX	Diclofenac2	19 Homo sapiens	-	simple assay module
<input type="checkbox"/>					6957	Effect of Nutritional Interventions on Inflammatory Status in Healthy Overweight Men (Foodmix)	35 Homo sapiens	Compound treatment, Oral Glucose Tolerance Test (OGTT), high fat post-prandial challenge	simple assay module, metabolomics
<input type="checkbox"/>					NuGO_PPSH	Human PPS: an intervention study	10 Homo sapiens	Fasting, Food intake	simple assay module, metabolomics
<input type="checkbox"/>					10 OAD	Identification of biomarkers and disease	262 Mus	Bodyweight, Compound treatment,	simple assay module

## 1.3 Import part of study design

Instead of walking through the wizard, GSCF also allows users to import a part of the study design. This can be a list of subjects, samples or events.

This is an example of importing subjects:

Click on Import > A part of the study design using the menu on top.



A screenshot of the GSCF interface. The top navigation bar includes 'Home', 'Create', 'Import' (with a dropdown menu), 'Export', 'Browse', 'Search', and 'Modules'. The 'Import' dropdown menu is open, showing three options: 'A complete study with straightforward design', 'A part of the study design' (which is highlighted with a green oval), and 'A list of studies (choose Study)'. The main content area on the left contains an 'Introduction' to GSCF, mentioning its use for capturing study designs and its compatibility with various study types. On the right, there is a 'Quicksearch' bar with a 'Search term' input field and a 'Quick Start' section with a brief description of how to use the 'studies' menu to create studies or study data.

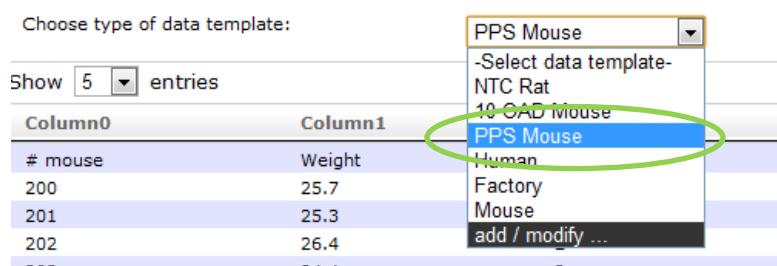
### Step 1: Import file

Select your excel file. The excel sheet should have this format: every study, subject, sample or event has its own row.

- It does not matter in *what column* which information is stored, as you can map the field in the template on the columns in your excel sheet.
- It does not matter *how many headers* are included in your excel sheet, as you can define in which row the first subject/ sample or event can be found.

	A	B	C	D	E
1	# mouse	Weight	Cage number	Number of mice in cage	
2	200	25.7	1	2	
3	201	25.3	1	2	
4	202	26.4	2	2	
5	203	24.4	2	2	
6	204	24.2	3	3	

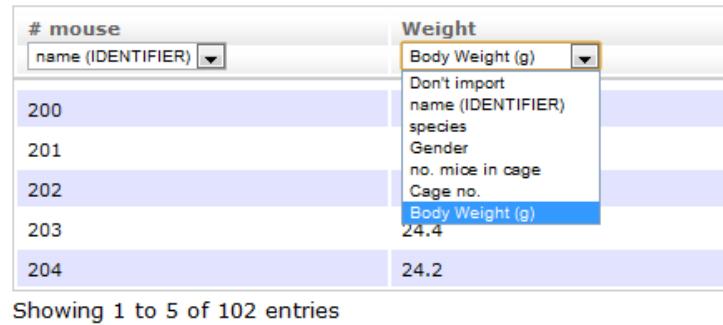
Make sure to select the correct data template; e.g. a mouse subject template for a mouse study. The importer will show a preview of your uploaded excel file.



A screenshot of the 'Choose type of data template:' interface. The dropdown menu shows 'PPS Mouse' as the selected option. A list of other templates is shown in a dropdown menu, with 'PPS Mouse' highlighted with a green oval. Below the dropdown is a preview table showing columns 'Column0' and 'Column1' with data rows for mice 200, 201, 202, and 203.

## Step 2: Assign properties

Map the information in your excel sheet on the columns, using the dropdowns. If a certain field is missing, go to back to Step 1, where you can modify or add fields for a certain template.



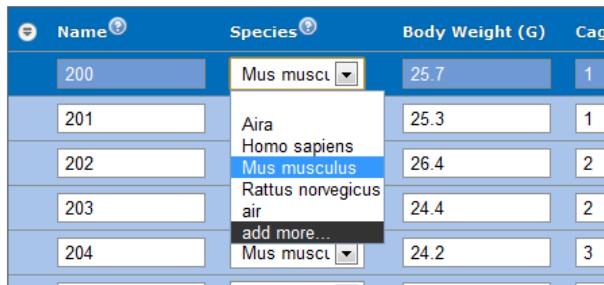
The screenshot shows a table with columns for '# mouse' and 'Weight'. The 'Weight' column has a dropdown menu open, showing options like 'Body Weight (g)', 'Don't import', 'name (IDENTIFIER)', 'species', 'Gender', 'no. mice in cage', 'Cage no.', and 'Body Weight (g)' again, with 'Body Weight (g)' selected. The table data includes rows for mice 200, 201, 202, 203, and 204, with their respective body weights.

# mouse	Weight
200	Body Weight (g)
201	Don't import
202	name (IDENTIFIER)
203	species
204	Gender
	no. mice in cage
	Cage no.
	Body Weight (g)
	24.4
	24.2

Showing 1 to 5 of 102 entries

## Step 3: Add information

Add information to the table when necessary. Multiple rows can be selected by click and dragging.



The screenshot shows a table with columns for 'Name', 'Species', 'Body Weight (G)', and 'Cag'. The 'Species' column has a dropdown menu open, showing options like 'Mus muscul', 'Aira', 'Homo sapiens', 'Mus musculus', 'Rattus norvegicus', 'air', 'add more...', and 'Mus muscul', with 'Mus musculus' selected. The table data includes rows for mice 200, 201, 202, 203, and 204, with their respective species and body weights.

Name	Species	Body Weight (G)	Cag
200	Mus muscul	25.7	1
201	Aira	25.3	1
202	Homo sapiens	26.4	2
203	Mus musculus	24.4	2
204	Rattus norvegicus	24.2	3

## Step 4: Confirmation

Check whether the information is correctly mapped and click > Next. Click on the study title to view your imported study data.



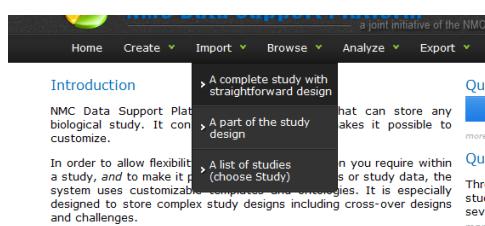
The screenshot shows a 'Show Study' interface with tabs for 'Study Information', 'Subjects', 'Events timeline', 'Events table', 'Assays', and 'Samples'. The 'Subjects' tab is active, displaying a table with columns for 'name', 'species', 'Body Weight (g)', and 'Cage no.'. The table data matches the information entered in Step 3.

name	species	Body Weight (g)	Cage no.
200	Mus musculus	25.7	1
201	Mus musculus	25.3	1
202	Mus musculus	26.4	2
203	Mus musculus	24.4	2

## How to import my own samples and samplenames?

This chapter will show you how to import your own samples and sample names.

Start with Import > A complete study with straightforward design. This will start a short wizard.



Define basic information of your study, and click next. Arrows indicate required fields:

New study (step 1 of 4)

Define the basic properties of your study  
Enter all the basic information of your study. Keep in mind that the more specific the information that is filled out, the more valuable the system will be.

Template	demo														
Title	demo														
Description	demostudy														
Code	description														
Start Date	01/03/2012														
Blob	<input type="button" value="Upload"/>														
Publications	No publications selected <input type="button" value="Add Publication"/>														
Contacts	null, Edo / Demoman <input type="button" value="Add Contact"/>														
Authorization	<table border="1"> <tr> <td>Public</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Published</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Readers</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Add User</td> <td><input type="button" value="Add User"/></td> </tr> <tr> <td>Writers</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Administrators</td> <td><input type="checkbox"/></td> </tr> <tr> <td>Add User</td> <td><input type="button" value="Add User"/></td> </tr> </table>	Public	<input type="checkbox"/>	Published	<input type="checkbox"/>	Readers	<input type="checkbox"/>	Add User	<input type="button" value="Add User"/>	Writers	<input type="checkbox"/>	Administrators	<input type="checkbox"/>	Add User	<input type="button" value="Add User"/>
Public	<input type="checkbox"/>														
Published	<input type="checkbox"/>														
Readers	<input type="checkbox"/>														
Add User	<input type="button" value="Add User"/>														
Writers	<input type="checkbox"/>														
Administrators	<input type="checkbox"/>														
Add User	<input type="button" value="Add User"/>														

Choose the excel file with appropriate subject and sample data, for example:

A	B	C	D	E	F	G	H	I
1 SubjectID	SampleName	Label	Strain	genotype	Gender	name_old	starttime	endtime
2 L_022	L_22_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLR/-	Male	22	0w	0w
3 L_041	L_41_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLR/-	Male	41	0w	0w
4 L_050	L_50_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLR/-	Male	50	0w	0w
5 L_076	L_76_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLR/-	Male	76	0w	0w
6 L_077	L_77_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF	C57BL/6	LDLR/-	Male	77	0w	0w

Describe your subjects, samples and events, by using existing templates:

Excel file to import:  Uploaded dbnp link array2 events.xls

Subject template: Human subjects

Event template: - no event template -

Sampling event template: Blood sampling

Sample template:

The important step during import is to map your columns with GSCF terms, to indicate how your excel sheet is structured. Any data you want to skip can be indicated by selecting 'Don't import'.

For example, choose subject name where your subject IDs and 'sample name [identifier]', where your sample names are:

Imported file (step 2 of 4)

Assign columns to template fields  
You uploaded: dbnp link array2 events.xls. This list shows the first 5 rows of the uploaded file for reference. The excel file with the fields in the database.

Excel columns	SubjectID	SampleName	Label
Example data	L_022	L_22_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF
	L_041	L_41_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF
	L_050	L_50_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF
	L_076	L_76_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF
	L_077	L_77_OrganSampling_Ldr_9whf_9wLiver	LDLR_9wHF

Template field:

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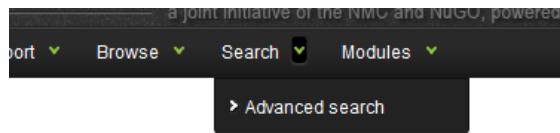
Fill in missing values, and select assays if you wish. The wizard will then give a study summary. After 'Save', you can view your study:

Show Study

Study Information	Subjects	Events timeline	Events table	Assays	Samples	Persons	Publications
<b>Parent Subject</b>	<b>Parent Sampling Event</b>	<b>Parent Event Group</b>	<b>name</b>				
L_103	Blood sampling at 0 seconds		L_103_OrganSampling_Ldrl_9whf_9wLiver				
L_120	Blood sampling at 0 seconds		L_120_OrganSampling_Ldrl_9whf_9wLiver				
L_201	Blood sampling at 0 seconds		L_201_OrganSampling_Ldrl_16whf_16wLiver				
L_202	Blood sampling at 0 seconds		L_202_OrganSampling_Ldrl_16whf_16wLiver				
L_203	Blood sampling at 0 seconds		L_203_OrganSampling_Ldrl_16whf_16wLiver				
L_204	Blood sampling at 0 seconds		L_204_OrganSampling_Ldrl_16whf_16wLiver				
L_205	Blood sampling at 0 seconds		L_205_OrganSampling_Ldrl_16whf_16wLiver				
L_206	Blood sampling at 0 seconds		L_206_OrganSampling_Ldrl_16whf_16wLiver				
L_207	Blood sampling at 0 seconds		L_207_OrganSampling_Ldrl_16whf_16wLiver				
L_208	Blood sampling at 0 seconds		L_208_OrganSampling_Ldrl_16whf_16wLiver				
L_209	Blood sampling at 0 seconds		L_209_OrganSampling_Ldrl_16whf_16wLiver				
L_210	Blood sampling at 0 seconds		L_210_OrganSampling_Ldrl_16whf_16wLiver				

## 2. Advanced search

Data from GCSF and the assay modules can be queried by using the Advanced search. Use the menu on top of the page and click on Search > Advanced search.



On this page you can search for *any of the parameters/fields used in GCSF and the modules*. This can be Age, Subject Name, Cholesterol (or other feature names used in Simple Assay module), or Classification (or other fieldnames used in Metagenomics module).

*Search example: Let's assume you want to have a list of all blood samples, where subjects are of age 30 or higher (among all your studies). First, you have to specify parameters. Note that while you type for a fieldname, you will get a list of possible fieldnames that exist in the database:*

### Search database

#### 1 Select criteria

N.B. Comparing numerical values is done without taking into account the units. E.g. a weight of 1 kg equals 1 grams.

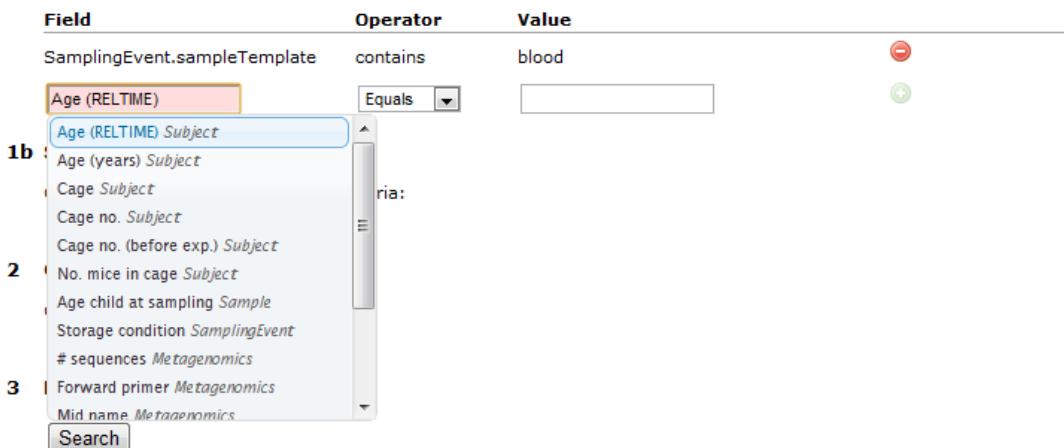
Field	Operator	Value
SamplingEvent.sampleTemplate	contains	blood
Age (RELTIME)	Equals	

1b: Age (years) Subject

2: No. mice in cage Subject

3: Forward primer Metagenomics

Search



Choose your output format: results can be shown on either study-, sample or assay level.

#### 2 Output type

Choose the type of output:

Samples

Studies

3 Samples

Assays

Search

Click Search, and you will get a list of all the samples that match to the specified criteria. Results of this search can be exported, for example as CSV file.

#### Query results: Sample search 1

2801 samples found with samplingevent.sampletemplate contains blood and subject.age (reltime) >= 30

	Name	Study	SamplingEvent sampleTemplate	Subject Age (RELTIME)
<input type="checkbox"/>	1029-49_Blood_2b_0sTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w15mTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w1hTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w1s	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w2hTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w30mTailBlood	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w3dBloodSacrifice	PPS1	Blood sacrifice	12w
<input type="checkbox"/>	1029-49_Blood_2b_1w45m	PPS1	Tail blood	12w
<input type="checkbox"/>	1029-49_Blood_All_-2w3d10hTailBlood	PPS1	Tail blood	12w

Showing 1 to 10 of 2,801 entries

[First](#) [Previous](#) [1](#) [2](#) [3](#) [4](#) [5](#) [Next](#) [Last](#)

[Search within results](#)  
 [Refine by classification \(Metagenomics\)](#)  
 [Search again](#)  
 [Discard results](#)  
 [Previous searches](#)

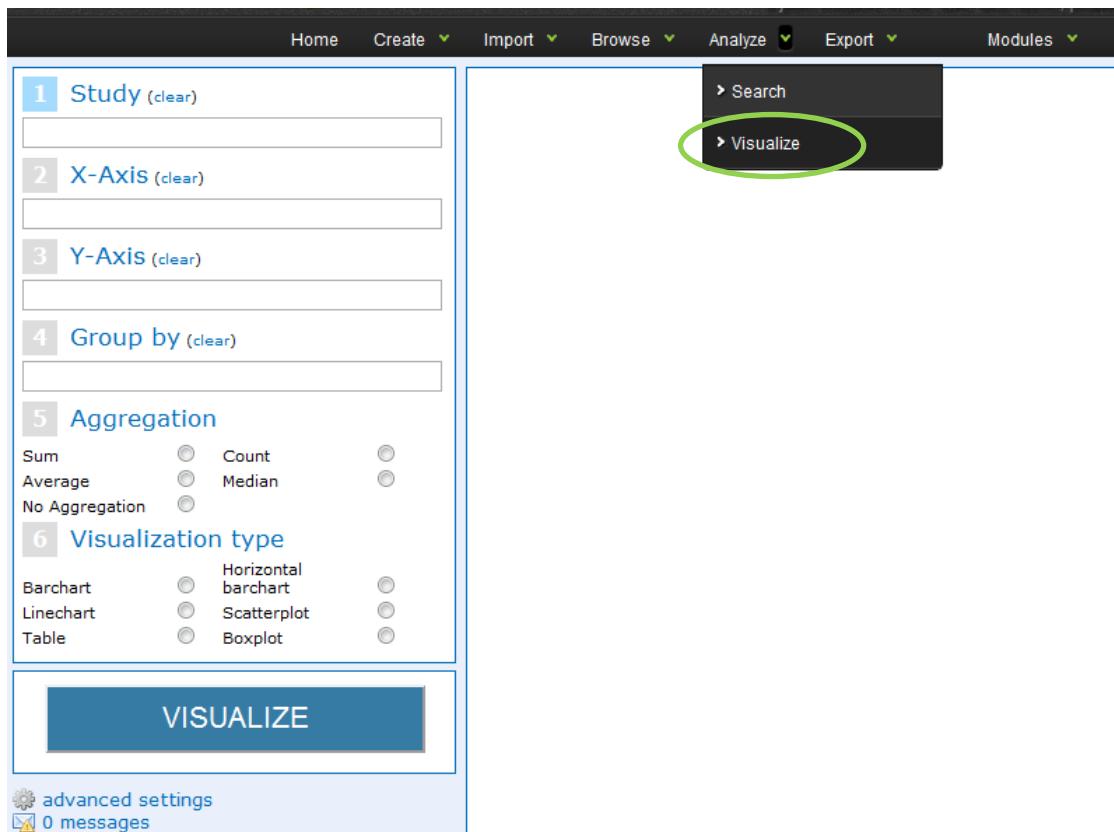
[Export as CSV](#)  
 [Export as fasta \(Metagenomics\)](#)  
 [Export metadata \(Metagenomics\)](#)

- Note: especially when you choose *sample* as the output format, this search can take several minutes, since the number of samples can be very high.

### 3. Visualize

The visualization tool GSCF allows you to visualize any data that is entered into the database. This can be subject-related data (such as weight, BMI or average age), but also SAM data (such as average leptin-levels measured, grouped by event group).

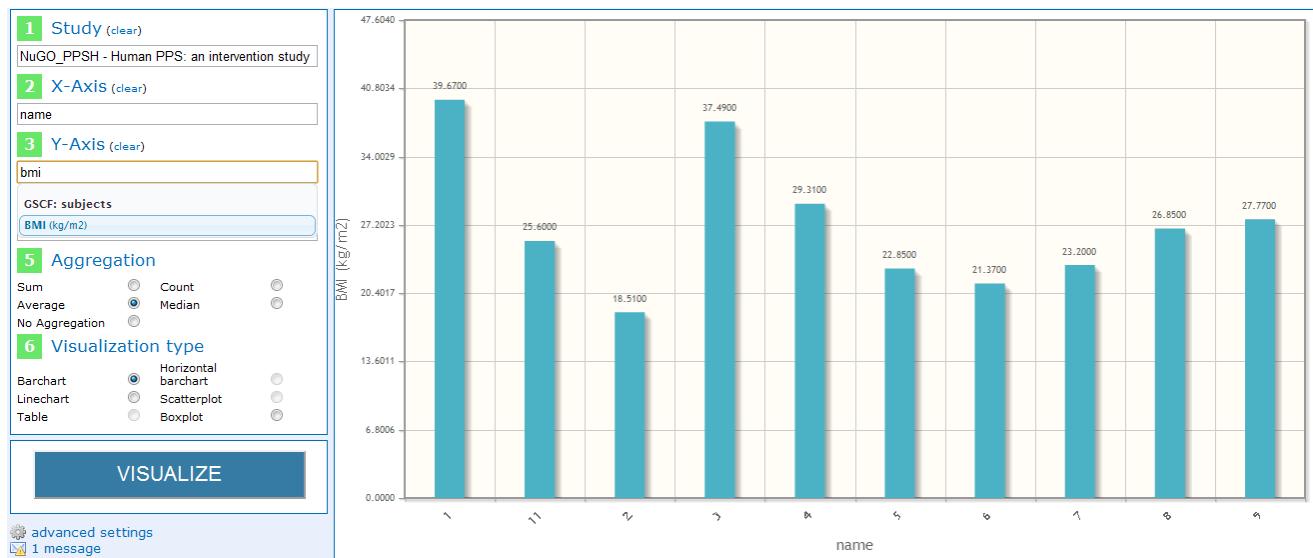
To enter the visualization tool, go to Analyze > Visualize, and you will see the control panel for visualizations on the left:



### 3.1 How to get GSCF data visualized?

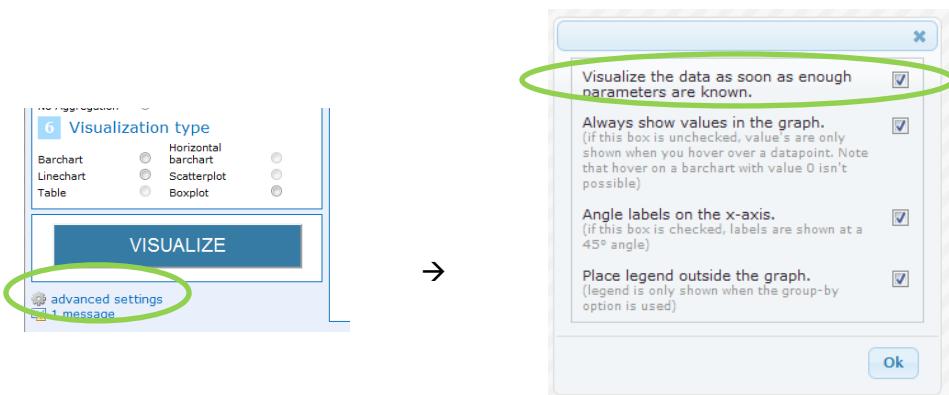
First, select your study and choose parameters for the X- and Y-axis. You can use the search bar and just type the field you want to use. The Group by functionality is optional, so you can leave this unchanged.

Step 5 will allow you to specify how to aggregate the data, but average is selected by default. If there are multiple visualization types possible, you have to indicate how you want to view it. If all parameters are set, the graph will automatically be generated.



Below the 'Visualize' button there are links for advanced settings and messages. If your data is invalid to be visualized, or cannot be found, a message will appear. Click on the link to read the full message.

Click on advanced settings for more interface options. Especially with studies that have a lot of data, the first item is important: by default the tool will show a graph as soon as enough parameters is known. To visualize a graph manually deselect this item:



## 3.2 How to get module data visualized?

Instead of GSCF fields, you can also select fields from the modules that you have entered data into. For instance, you can select a feature from SAM (simple assay module), by selecting this on the Y-axis. All features are grouped together by assay name.

You can also type the assay name to see what features are possible:



### Aggregation

Several aggregation options are possible. By default 'Average' is selected, however you can choose any of the options that are enabled. The graph will reload when you choose another type of calculation of your data.

### Visualization types

The tool enables you to visualize your data in different kinds. Depending on the type of data you selected, the types are functional. For example, if you choose to have categorical data on the X-axis (e.g. event group name, or subject number) you cannot choose for a scatterplot.

#### VISUALIZATION TYPES

X-AXIS	Y-AXIS	TYPE
Numerical	Numerical	Scatterplot, Linechart
Numerical	Categorical	Horizontal Barchart
Categorical	Numerical	Barchart, Linechart
Categorical	Categorical	Table

## 4. Export data

Both GSCF as well as Assay data can be exported.

### 4.1 Export GSCF data

A whole study with GSCF data can be exported as a SimpleTox Excel file. To do this, navigate to Export > Export studies as SimpleTox Excel file. Select which studies you want to export, and click Export. The output will look like this:

	A	B	C	D	E	F	G	H	I	J	K	L	C
1	SubjectID	DataFile	HybName	SampleName	ArrayType	Label	StudyTitle	Array_ID	Species	name	species	Body Weight	Category
2	Subject 6			Subject6_WholeBody control		PPS3			Mus musc	Subject 6	Mus musculus		
3	Subject 8			Subject8_WholeBody control		PPS3			Mus musc	Subject 8	Mus musculus		
4	Subject 5			Subject5_WholeBody control		PPS3			Mus musc	Subject 5	Mus musculus		
5	Subject 7			Subject7_WholeBody control		PPS3			Mus musc	Subject 7	Mus musculus		
6	Subject 10			Subject10_WholeBod control		PPS3			Mus musc	Subject 10	Mus musculus		
7	Subject 3			Subject3_WholeBody Minocyclin	PPS3				Mus musc	Subject 3	Mus musculus		
8	Subject 9			Subject9_WholeBody Minocyclin	PPS3				Mus musc	Subject 9	Mus musculus		
9	Subject 1			Subject1_WholeBody control		PPS3			Mus musc	Subject 1	Mus musculus		
0	Subject 4			Subject4_WholeBody Minocyclin	PPS3				Mus musc	Subject 4	Mus musculus		
1	Subject 2			Subject2_WholeBody control		PPS3			Mus musc	Subject 2	Mus musculus		
2	Subject 16			Subject16_WholeBod HF-AL		PPS3			Mus musc	Subject 16	Mus musculus		
3	Subject 12			Subject12_WholeBod chF		PPS3			Mus musc	Subject 12	Mus musculus		
4	Subject 17			Subject17_WholeBod chF		PPS3			Mus musc	Subject 17	Mus musculus		
5	Subject 14			Subject14_WholeBod HF-AL		PPS3			Mus musc	Subject 14	Mus musculus		
6	Subject 13			Subject13_WholeBod HF-AL		PPS3			Mus musc	Subject 13	Mus musculus		
7	Subject 20			Subject20_WholeBod Chow		PPS3			Mus musc	Subject 20	Mus musculus		

### 4.2 Export Assay data

If you want to export a study, but also the data from the assays that belong to this study, use Export > Export Assay data to file. This will allow you to export measurements from SAM, for example.

Select the study and assay for export and Submit.

Select the assay you want to export data from

With this exporter you can export (meta) data about samples from an assay to a file. First, select a study from the first list and then select an assay from that study from the second list.

Human PPS: an intervention study

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In the next screen you can specify in more detail which fields you want to export. If you want to export SAM Assay data, make sure that Measurements is checked:

Select the columns that you want to be included in the resulting file

In this step you can make a selection from the available fields stored in the database a module (if available).

Subject Data  
 name   
 species   
 Gender  
 Age (RELTIME)  
 Body Weight (g)  
 Cage  
 no. mice in cage  
 Cage no.  
 Sampling Event Data  
 startTime   
 duration   
 sampleTemplate   
 Control  
 Sample Data  
 name  
 Event Group  
 name   
 Measurements  
 Cholesterol

Finally, select the file type. All types can be opened in Excel.

Select type of resulting file

- Tab delimited (.txt)
- Comma Separated: USA/UK (.csv)
- Semicolon Separated: European (.csv)

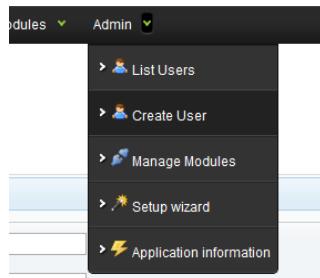
## 5. Access control

### 5.1 Admin and users

GSCF makes a distinction between administrators and users. When a new user registers, he or she will automatically become a normal user. When a new user is added by the administrator, he can give this user either normal user rights, or an administrator role.

#### *How to create a new user or admin?*

Go to Admin > Create User



All three, username, password and email address are required fields. To finish this user, make sure User confirmed and Admin confirmed are checked, and click Save.

A screenshot of the 'Create User' form. The form has two tabs: 'User info' (selected) and 'Roles'. The 'User info' tab contains fields for 'Username' (user), 'Password' (redacted), 'Email address' (user@dbnp.org), 'User confirmed' (checked), 'Admin confirmed' (checked), 'Account expired' (unchecked), 'Account locked' (unchecked), and 'Password expired' (unchecked). A green oval highlights the 'User info' section. At the bottom are 'Save' and 'Cancel' buttons, and a copyright notice: 'Copyright © 2008 - 2011 NuGO, NMC and NBIC. All rights reserved. For more information go to [www.nugoid.org](#)'.

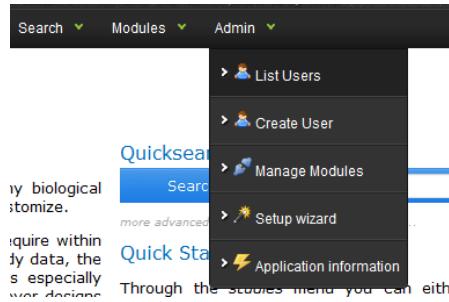
#### *How to give a user administrator rights?*

Only after a user has been created, the option of giving administrator rights is enabled. This can be found in the Roles tab, while editing a user:

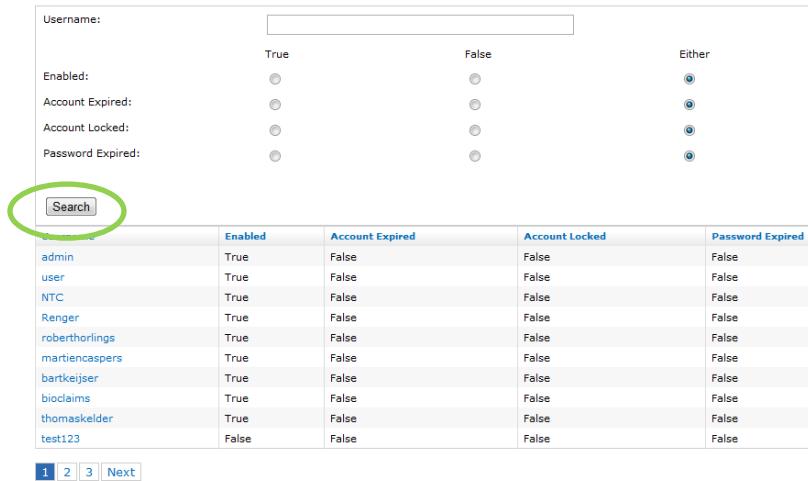
A screenshot of the 'Edit User' form. The 'User info' tab is selected. The 'Roles' tab is shown as a separate tab. Below the tabs, there is a checkbox labeled 'ROLE\_ADMIN' which is unchecked. At the bottom are 'Save' and 'Delete' buttons, and a copyright notice: 'Copyright © 2008 - 2011 NuGO, NMC and NBIC. All rights reserved. For more information go to [www.nugoid.org](#)'.

## How to see all users and their access rights?

Go to Admin > List Users



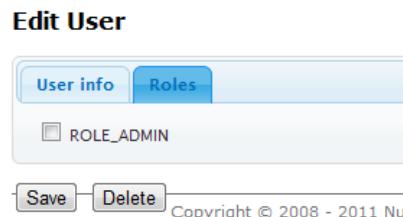
You will enter a search page, but if you search without any given character for username, you get a full list of all known users and administrators:



Username:	Enabled	Account Expired	Account Locked	Password Expired
Enabled:	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Account Expired:	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Account Locked:	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
Password Expired:	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
<b>Search</b>				
admin	True	False	False	False
user	True	False	False	False
NTC	True	False	False	False
Renger	True	False	False	False
roberthorlings	True	False	False	False
martencaspers	True	False	False	False
bartkeijser	True	False	False	False
bioclaims	True	False	False	False
thomaskelder	True	False	False	False
test123	False	False	False	False

1 2 3 Next

To see the role for a certain user name, click on that name, and go to the tab Roles. Here you can see if this user has admin rights.



**Edit User**

User info Roles

ROLE\_ADMIN

Save Delete

## 5.2 Readers and writers

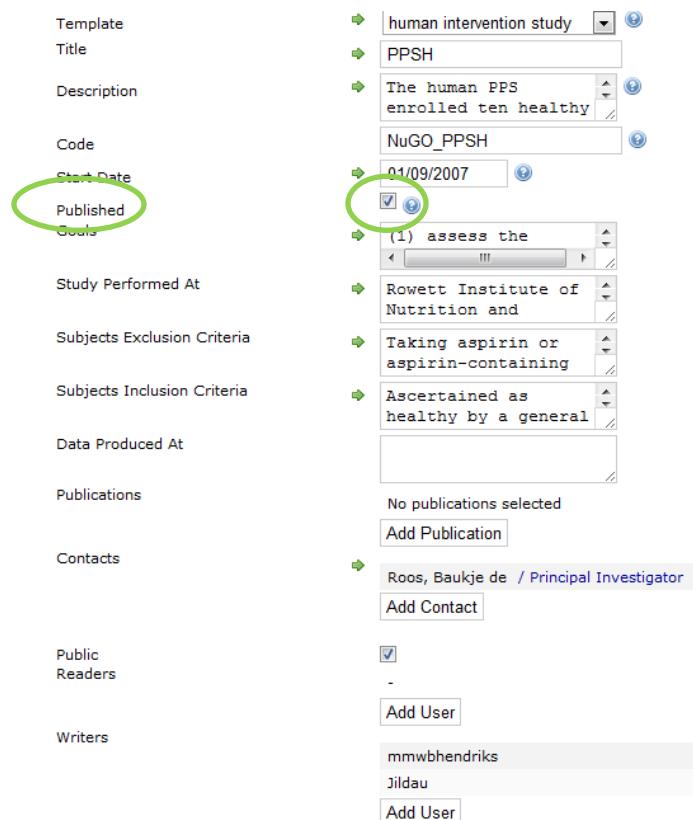
When a new study is created, other users can become Reader or Writer of that study. Readers are able to see the study, but cannot edit it. Writers can also edit the study. Before you assign Readers and Writers, make sure your study is published first.

### How to publish a created study?

Before a study is actual visible to study readers and writers, make sure that the box Published is checked. This can be done in the first page of the study create Wizard.

This determines whether this study is published (accessible for the study readers and, if the study is public, for anonymous users). A study can only be published if it meets certain quality criteria, which will be checked upon save.

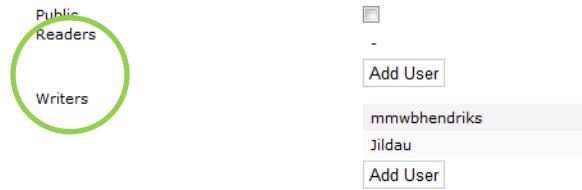
The option is maybe a bit hidden and easily skipped, but can be found here:



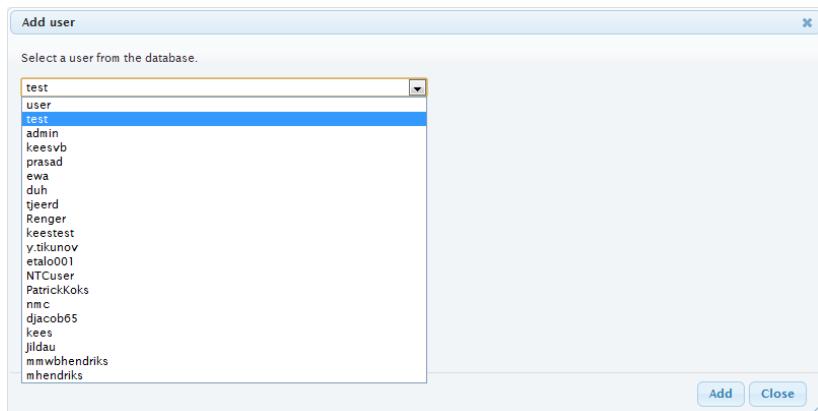
The screenshot shows the 'Goals' section of a study creation wizard. On the left, there is a list of fields: Template, Title, Description, Code, Start Date, Published, Goals, Study Performed At, Subjects Exclusion Criteria, Subjects Inclusion Criteria, Data Produced At, Publications, Contacts, Public Readers, and Writers. The 'Published' field is highlighted with a green circle. To its right is a dropdown menu showing 'human intervention study' and a checked checkbox labeled '(1) assess the'. Below this are sections for 'Study Performed At', 'Subjects Exclusion Criteria', 'Subjects Inclusion Criteria', 'Data Produced At', 'Publications', 'Contacts', 'Public Readers', and 'Writers'. The 'Public Readers' section shows a checked checkbox and a list of users: 'mmwbhendriks' and 'Jildau'. The 'Writers' section shows a list of users: 'mmwbhendriks' and 'Jildau'.

## How to add users as readers or writer of a study?

In the first step of the study create wizard, you can assign users as public Readers or as Writers of the study.



Click on Add User, and select the user you want to become a Reader, and click on Add to add this person as Reader. Follow the same procedure for Writers, to assign a user as Writer.



## How to see Readers and Writers of a study?

To see who are Readers or Writers of a study, go to the study list (Browse > All Studies) and view a study. On the first tab, Study Information, you can see a list of the study owner, and the assigned Readers and Writers:

Show Study

Study Information Subjects Events timeline Events table Assays Samples Persons Publications

title	Human PPS: an intervention study
description	The human PPS enrolled ten healthy volunteers that were asked to come to the Human Nutrition Unit in Aberdeen on four different days of the week during four weeks after an overnight fast to provide a blood sample (for the isolation of plasma, platelets and PBMC), and a saliva and a morning urine sample to assess intra- and interindividual variations in baseline levels. On the fourth sampling day, volunteers were fasted for an additional 24 h (total of 36 h) and again plasma, saliva and urine samples as well as circulating blood cells were collected for transcriptome, proteomic and metabolomic analysis. Biomarkers of biological variability and metabolic responses are being monitored in plasma, platelets, peripheral blood mononuclear cell (PBMC), urine and saliva by proteomics based on 2D-gel based platforms coupled to mass spectrometry for protein identification. Alterations in the PBMC transcriptome are being assessed by microarray analysis. Biomarker detection and identification is being achieved by metabolomics. Biomarker detection is achieved based on NMR, GC-MS, GC-MS/MS and LC-MS/MS platforms comprising non-targeted and targeted approaches. Moreover, a panel of 89 hormones, cytokines and chemokines and metabolic factors was analyzed on a commercial targeted profiling platform (RulesBasedMedicine, www.rulesbasedmedicine.com). In this unique combination of nutrigenomics tools this study should provide the most comprehensive metabolic phenotyping possible in human volunteers with minimal invasive methods for obtaining appropriate biosamples.
code	NuGO_PPS
startDate	2007-09-01 00:00:00.0
published	true
Objectives	(1) assess the biological intra- and inter-individual variance of a huge spectrum of molecular, metabolic and clinical parameters employing the different omics technologies at baseline and after a 36 h fasting period, (2) identify common and unique changes in these parameters in response to fasting, (3) determine the most comprehensive and sensitive omics approaches to detect and quantify the effects of a nutritional fasting challenge in humans.
Institute	Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen
Consortium	NuGO
objective related inclusion criteria	Ascertained as healthy by a general medical examination including an haemotinic assessment
objective related exclusion criteria	Taking aspirin or aspirin-containing drugs, other anti-inflammatory drugs, or any drugs or herbal medicines known to alter platelet function or the haemostatic system in general.
Events	Fasting, Food intake
Sampling events	Blood, Saliva, Urine after fasting
Public	None
Owner	user
Readers	jsaito, metabolomics
Writers	-

## How to make a study publicly available?

If you want to make a study publicly readable, so even for non-DSP users, you can indicate this also in the first step. Make sure that Public is checked:

Template  

Title  

Description  

Code  

Start Date    

Published  

Goals  

Study Performed At  

Subjects Exclusion Criteria  

Subjects Inclusion Criteria  

Data Produced At  

Publications  

[Add Publication](#)

Contacts  

[Add Contact](#)



Writers  



[Add User](#)

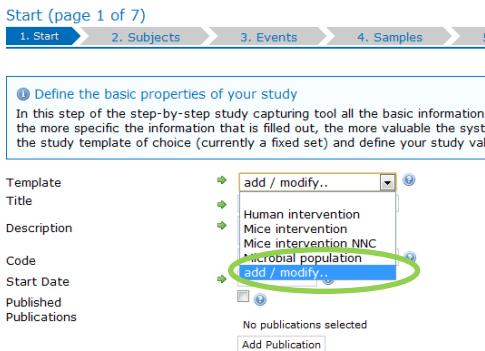
Public  
Readers

## 6. Templates

In order to allow flexibility to capture all information you require within a study, and to make it possible to compare studies or study data, the system uses customizable templates and ontologies. Templates are available at all steps of the create study wizard.

For example, to indicate the type of study design, choose an existing Study template, or 'add/modify templates'. This will show a popup where you can define the fields you want to appear next to default fields for study details:

Choose Add/Modify to add or edit templates:



Start (page 1 of 7)

1. Start 2. Subjects 3. Events 4. Samples

Define the basic properties of your study

In this step of the step-by-step study capturing tool all the basic information the more specific the information that is filled out, the more valuable the system template of choice (currently a fixed set) and define your study val

Template

Title

Description

Code

Start Date

Published

Publications

add / modify..

Human intervention

Mice intervention

Mice intervention NNC

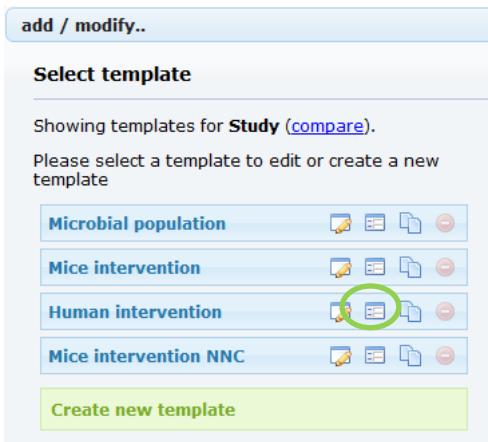
Microbial population

add / modify..

No publications selected

Add Publication

Now you can see a list of existing templates:



add / modify..

Select template

Showing templates for **Study** ([compare](#)).

Please select a template to edit or create a new template

Microbial population

Mice intervention

Human intervention

Mice intervention NNC

Create new template

By clicking the first icon you can change the name and description. For each template you can also describe additional fields. Click on the second icon to modify template fields.

In this screen you can create new fields, indicate what is required for these fields, and you can organize all fields:

**add / modify..**

**Human intervention (switch)**

Currently, this template contains the following fields.  
Drag fields to reorder. Drag fields to the list of available fields to remove the field from the template.

title (Short text)
description (Long text)
code (Short text)
startDate (Date)
published (True/false)
↳ Institute (Short text)  
↳ Consortium (Short text)  
↳ Objectives (Long text)  
↳ Study protocol (File)  
↳ Central conclusion (Long text)  
↳ objective related inclusion criteria  

**Available fields**

These fields are available for adding to the template.  
Drag a field to the template to add it.

Type (Dropdown selection of terms)   
------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

**Create new field**

Other parts within the GSCF study design that apply the template system are: Subjects (Species template), Events, Sampling Events, Samples and Assays.

## FAQs

### Where can I see a list of my studies?

Click on Browse > My studies to view your studies. It is possible that other users indicate you are reader of a study. These studies also appear in this list.

### Where can I update study information?

Click on Browse > My studies, and use the pencil on the left to edit a certain study. Just as creating a new study, this will start the study wizard. Using 'next' and 'previous' you can navigate through your study and update any information from this study.

### How can I import events, or sampling events?

Events or sampling events can be imported using a short wizard (the same way you can import subjects or samples, described in chapter 1.3). Use the following format if you want to import events. Describe starttime, endtime, and a column for event description (second Diet treatment).

Subjectname	starttime	endtime		Diet treatment	Diet treatment
N_134_ADEM	0s	12w	ADEM/134	A	Green tea
N_010_ADMA	0s	12w	ADMA/10	B	Placebo
N_123_AHIF	0s	12w	AHIF/123	B	Placebo
N_158_ALAN	0s	12w	ALAN/158	B	Placebo

Use Import> Import part of study design, choose your file and indicate where your data begins. If your excel sheet contains subject names, you can link these events to the subjects you have in GSCF:

Choose your Excel file to import:

Date format:

Use data from sheet:

Column header is at:

Choose type of data:   Attach Events to Existing Subjects

Choose your study:

Choose type of data template:

Show 5 entries

Column0	Column1	Column2	Column3	Column4	Column5	Column6
	Subjectname	sharvest		Diet treatment	Diet treatment	
	N_134_ADEM	storage		ADEM/134	A	Green tea
	ADMA / 010	compound treatment		ADMA/10	B	Placebo
	AHIF / 123	GC-MS analysis		AHIF/123	B	Placebo
	ALAN /158	sampling		ALAN/158	B	Placebo
		sampling - 2				
		diet				
		challenge				
		add / modify ...				

Showing rows 1 to 5 out of a total of 188 (in diet treatment)

[next >](#)

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The result is one event, in which all subjects take part:

Show Study

[Study Information](#) [Subjects](#) [Events timeline](#) [Events table](#) [Assays](#) [Samples](#) [Persons](#) [P](#)

Name	Events	Subjects
Diet_0s	diet (event) start time 0s	
		187 Homo sapiens

## *How can I add more samples to my study?*

Click on **Browse > My studies**, and use the pencil on the left to edit a certain study. Samples are created as a combination of a sampling event, a subject and an event group. Change any of these to your needs and this will create more samples.

For example, if you miss a certain subject, add this subject in Step 2. Then navigate by clicking 'next' and this subject can be selected into a certain eventgroup. By clicking 'next' GSCF now creates new samples based on the new subject that was added to an eventgroup.

## *How can I add more samples to an assay?*

See previous question how to add more samples into your study. Then go to Step 5, and click 'next'. Now you reach the in-between step, where you can add samples to an assay.

## *How are sample names created in GSCF?*

Each sample name created in GSCF is composed of several fields. For example, the name 11\_UrineAfterFasting\_AllPersons\_-1d has been created from:

Subject name: 11 Event group: All Persons

Sampling event: Urine After Fasting Starttime Sampling event: -1 day

If there are more samples with the same content, then sample names get the addition \_1, \_2, \_3.

*Can I change the sample names created by GSCF?*

Yes, you can change the names that are automatically created by GSCF. However, especially when you have a long list of samples, this has to be done all manually. Go to the Study Edit > Samples.

Another option is to import samples, and thereby use your own samplenames. During the import you can attach samples to corresponding subjects that you have in GSCF. See chapter 1, page 13, for more details on sample import.

## *Where can I search among multiple studies?*

Click on Search > Advanced Search. Select your GSCF fields and values you want to search for. Then select type of output (based on Studies, Samples or Assays).

For example, show me all samples from subjects that are at least 62 years of age;

Search database

### 1 Select criteria

N.B. Comparing numerical values is done without taking into account the unit.

Field	Operator	Value
Age (years)	>=	60
Age (RELTIME) Subject		
Age (years) Subject		
Cage Subject		
Cage no. Subject		
Cage no. (before exp.) Subject		
No. mice in cage Subject		
Age child at sampling Sample		
Storage condition SamplingEvent		

This will result in the following output:

Query results: Sample search 7			
38 samples found with subject.age (years) >= 60			
	Name	Study	Subject Ag (years)
<input type="checkbox"/>	18-144_Blood_Placebo_15w	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_0s	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-5	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-4	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60
<input type="checkbox"/>	18-144_Blood_Placebo_-8	Relation between reduction of the inflammatory status and glucose metabolism in healthy overweight men (Diclofenac)	60

### *My samples do not appear in the module. What can I do?*

For samples to appear in a module attached to GSCF, make sure you have selected the right module for this assay. For example, make sure you selected module Simple Assay Module when you trying to view samples in this module (SAM). Second, make sure the right samples are actually in this assay. You can check this by clicking 'next' in Step 5. Here you can see a list of which samples are in what assay.

If the right samples do not exist for this assay and module, add more samples: Samples are created as a combination of a sampling event, a subject and an event group. Change any of these to your needs and this will create more samples.

For example, if you miss a certain subject, add this subject in Step 2. Then navigate by clicking 'next' and this subject can be selected into a certain eventgroup. By clicking 'next' GSCF now creates new samples based on the new subject that was added to an eventgroup.